

1645

RAW SEQUENCE LISTING DATE: 05/19/2000
 PATENT APPLICATION: US/09/201,916A TIME: 12:37:02

Input Set : A:\DYOU17.001AUS.TXT
 Output Set: N:\CRF3\05182000\I201916A.raw

ENTERED

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4 <110> APPLICANT: Hope, Ralph Graham
5      Mclauchlan, John
7 <120> TITLE OF INVENTION: VIRAL THERAPEUTICS
10 <130> FILE REFERENCE: DYOU17.001AUS
12 <140> CURRENT APPLICATION NUMBER: 09/201916A
13 <141> CURRENT FILING DATE: 1998-12-01
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 630
21 <212> TYPE: DNA
22 <213> ORGANISM: Hepatitis C Virus
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (43)...(630)
28 <400> SEQUENCE: 1
29 ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca cc atg agc acg aat      54
30                                     Met Ser Thr Asn
31                                     1
33 cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag      102
34 Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
35 5                                     10                                     15                                     20
37 gac gtt aag ttc ccg ggt ggc cag atc gtt ggt gga gtt tac ttg      150
38 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
39                                     25                                     30                                     35
41 ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act      198
42 Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
43                                     40                                     45                                     50
45 tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca      246
46 Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
47                                     55                                     60                                     65
49 cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc      294
50 Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
51                                     70                                     75                                     80
53 ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc      342
54 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
55 85                                     90                                     95                                     100
57 agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg      390
58 Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Arg Ser
59                                     105                                     110                                     115
61 cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc'gat      438
62 Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
63                                     120                                     125                                     130
65 ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc      486
66 Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
67                                     135                                     140                                     145
69 agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat      534

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70 Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
71      150      155      160
73 gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc      582
74 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
75 165      170      175      180
77 ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac      630
78 Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
79      185      190      195
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 60
84 <212> TYPE: DNA
85 <213> ORGANISM: Hepatitis C Virus
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (1)...(60)
90 <223> OTHER INFORMATION: Corresponds to aa 125 to 144 of SEQ ID. No. 1
92 <400> SEQUENCE: 2
93 acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc      48
94 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
95 1      5      10      15
97 ggc gcc cct ctt      60
98 Gly Ala Pro Leu
99      20
102 <210> SEQ ID NO: 3
103 <211> LENGTH: 18
104 <212> TYPE: DNA
105 <213> ORGANISM: Hepatitis C Virus
107 <220> FEATURE:
108 <221> NAME/KEY: CDS
109 <222> LOCATION: (1)...(18)
110 <223> OTHER INFORMATION: Corresponds to aa 161-166 of SEQ ID. No. 1
112 <400> SEQUENCE: 3
113 ggt gtg aac tat gca aca      18
114 Gly Val Asn Tyr Ala Thr
115 1      5
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 1900
120 <212> TYPE: DNA
121 <213> ORGANISM: Human
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: (1)...(1900)
126 <223> OTHER INFORMATION: n = A,T,C or G
128 <400> SEQUENCE: 4
129 cgtcttcggg acgcgccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag      60
130 gaagaaaaat ggcacccgtt gcagttgac cacaaccgag tgtggtgact cgggtggtca      120
131 acctgccctt ggtgagctcc acgtatgacc tcatgtcttc agcctatctc agtacaaagg      180
132 accagtatcc ctacctgaag tctgtgtgtg agatgscaga gaacggtgtg aagaccatca      240
133 cctccgtggc catgaccagt gctctgcccc tcatccagaa gctagagccg caaattgcag      300

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134 ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360
135 atcagccatc aactcagatt gttgccaatg ccaaaggcgc tgtgactggg gcaaaagatg 420
W--> 136 ctgtgacgac tactgtgact ggggccaaagg attctgtngc cagcacgacg acaggggtga 480
137 tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagtg 540
138 gcagcattaa cacagtcttg gggagtggga tgatgcagct cgtgagcagt ggcgtagaaa 600
139 atgcactcac caaatcagag ctgttggtag aacagtacct ccctctcact gaggaagaac 660
140 tagaaaaaga agcaaaaaaa gttgaaggat ttgatctggg tcagaagcca agttattatg 720
141 ttagactggg atcccgtgtc accaagcttc actcccgtgc ctaccagcag gctctcagca 780
142 ggggttaaga agctaagcaa aaaagccaac agaccatttc tcagctccat tctactgttc 840
143 acctgattga atttgccagg aagaatgtgt atagtgccaa tcagaaaatt caggatgctc 900
144 aggataagct ctacctctca tgggtagagt ggaaaaggag cattggatat gatgatactg 960
145 atgagtccca ctgtgctgag cacattgagt cactgtactc tgcaattgcc cgcaacctga 1020
146 ctacgacgct ccagaccacg tgccacaccc tcctgtccaa catccaaggt gtaccacaga 1080
147 acatccaaga tcaagccaag cacatggggg tgatggcagg cgacatctac tcagtgttcc 1140
148 gcaatgctgc ctccctttaa gaagtgtctg acagcctcct cacttctagc aaggggcagc 1200
149 tgcagaaaat gaaggaatct ttagatgacg tgatggatta tcttgttaac aacacgcccc 1260
150 tcaactggct ggtaggtccc ttttatcctc agctgactga gtctcagaat gctcaggacc 1320
151 aaggtgcaga gatggacaag agcagccagg agaccagcgc atctgagcat aaaactcatt 1380
152 aaacctgccc ctatcactag tgcagtctgt ggccagacag atgacacctt ttgttatgtt 1440
153 gaaattaaact tgctaggcaa ccctaaattg ggaagcaagt agctagtata aagggccctc 1500
154 attgtagtgt tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
155 ctgttcacct ggtaagaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
156 aaaattcaaa tgcacttatg ttctcattct atggccattg tgttgcctct gttactgttt 1680
157 gtattgaata aaaacatctt catgtgggct ggggtagaaa ctggtgtctg ctctggtgtg 1740
158 atctgaaaag gcgtcttcac tgctttatct catgatgctt gcttgtaaaa ctgattttta 1800
159 gtttttcatt tctcaaatag gaatactacc tttgaattca ataaaaattca ctgcaggata 1860
W--> 160 gaccagttna gnagcaaaac nncangtaca cnnaaganac 1900
162 <210> SEQ ID NO: 5
163 <211> LENGTH: 437
164 <212> TYPE: PRT
165 <213> ORGANISM: Human
167 <220> FEATURE:
168 <221> NAME/KEY: VARIANT
169 <222> LOCATION: (1)...(437)
170 <223> OTHER INFORMATION: Xaa = Any Amino Acid
172 <400> SEQUENCE: 5
173 Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
174 1 5 10 15
175 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
176 20 25 30
177 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
178 35 40 45
W--> 179 Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
180 50 55 60
181 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp
182 65 70 75 80
183 Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
184 85 90 95
185 Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val

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186          100          105          110
187 Thr Gly Ala Lys Asp Ala Val Thr Thr Val Thr Gly Ala Lys Asp
188          115          120          125
189 Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
190          130          135          140
191 Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
192 145          150          155          160
193 Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
194          165          170          175
195 Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro
196          180          185          190
197 Leu Thr Glu Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
198          195          200          205
199 Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
200          210          215          220
201 Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
202 225          230          235          240
203 Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
204          245          250          255
205 Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
206          260          265          270
207 Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
208          275          280          285
209 Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
210          290          295          300
211 His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
212 305          310          315          320
213 Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro
214          325          330          335
215 Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp
216          340          345          350
217 Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp
218          355          360          365
219 Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser
220          370          375          380
221 Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp
222 385          390          395          400
223 Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln
224          405          410          415
225 Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser
226          420          425          430
227 Glu His Lys Thr His
228          435
230 <210> SEQ ID NO: 6
231 <211> LENGTH: 31
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: A branched peptide containing residues 5-27 of the

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Input Set : A:\DYOU17.001AUS.TXT
Output Set: N:\CRF3\05182000\I201916A.raw

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237 HCV core protein.
239 <221> NAME/KEY: VARIANT
240 <222> LOCATION: (1)...(31)
241 <223> OTHER INFORMATION: Xaa = Ala or Pro at position 1, and Ile or Asn at
242 position 12.
244 <400> SEQUENCE: 6
245 Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln
246 1 5 10 15
247 Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Ala
248 20 25 30
250 <210> SEQ ID NO: 7
251 <211> LENGTH: 11
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
257 protein deletion plasmids.
259 <400> SEQUENCE: 7
260 gctgagatct a 11
262 <210> SEQ ID NO: 8
263 <211> LENGTH: 29
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
269 protein deletion plasmids.
271 <400> SEQUENCE: 8
272 gtaaccttcc tggttgctct tgagatcta 29
274 <210> SEQ ID NO: 9
275 <211> LENGTH: 17
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
281 protein deletion plasmids.
283 <400> SEQUENCE: 9
284 gtaacctttg agatcta 17
286 <210> SEQ ID NO: 10
287 <211> LENGTH: 18
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
293 protein deletion plasmids.
295 <400> SEQUENCE: 10
296 ctggcgcatt gagatcta 18
298 <210> SEQ ID NO: 11
299 <211> LENGTH: 28
300 <212> TYPE: DNA

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VERIFICATION SUMMARY

DATE: 05/19/2000

PATENT APPLICATION: US/09/201,916A

TIME: 12:37:03

Input Set : A:\DYOU17.001AUS.TXT

Output Set: N:\CRF3\05182000\I201916A.raw

L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6